



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/501,525

DATE: 07/22/2004

TIME: 11:16:06

Input Set : A:\PTO.YF.txt

Output Set : N:\CRF4\07222004\J501525.raw

3 <110> APPLICANT: GENFIT SA

5 <120> TITLE OF INVENTION: Method for identifying substances capable of modulating adipocyte

6 differentiation

8 <130> FILE REFERENCE: B0097WO

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/501,525

C--> 11 <141> CURRENT FILING DATE: 2004-07-16

13 <160> NUMBER OF SEQ ID NOS: 4

15 <170> SOFTWARE: PatentIn Ver. 2.1

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 1999

19 <212> TYPE: DNA

20 <213> ORGANISM: Homo sapiens

22 <400> SEQUENCE: 1

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 25 cctaagaagc ttccatcccc tccatgaccc aagccctcta acatgataga tctcctctac 180
 26 ttgagatctg ttattactca tgggacagtt gctgctctga agcgaaatac tggctgtttt 240
 27 ttgtttgttt gttttggaga cagagtctca ctctatcccc agggcggagt gcaatggcga 300
 28 tctcggctca ctgcaacctc cacctcccgg gttctagcga ttctcctgcc tcagcctcct 360
 29 gactagctgg gattacaggc acccaccacc acatccggct aatttttgta tttttagtag 420
 30 agacgtgggt tcaccgtggt ggtcaggctg gtctcaaaact cctgacctca ggtgatcaac 480
 31 ccacctcagc ctcacaaagt gctgggatta caggcatgag ccaaagcacc cggcaatgct 540
 32 ggctgtttct aaccctgtt cagtatttca cttgtacatc taccacacct cccattcggg 600
 33 gtgggcagat gaaactagca atggacgtct gaccttgggt cggtcacttc tcctaagctt 660
 34 cctgttcccc actagtaaaa agagggaggc ttaagatgat ctacatgttc ccctctgagt 720
 35 agtaatcttc tgtggaattc atattttatc ctccagcacc gaggggcagg ggtgtcactc 780
 36 tgccccacc ccctgcctca cctcttcccc attactttag gacctcaaag cactttcact 840
 37 attagttccc ctctgttgtc ctttttattt cccagacaaa gggaaatgac tcaccccaa 900
 38 gtcaactgga gtgggtggaa tgggtgcaat acaagcaaac agggagtccc tacagacatc 960
 40 cctacctctg tgggaactcc ttcccctgga ggtgttctcc ctaaggcgag tagaaggga 1020
 41 agggggtcac atttcctttc cttctctgga ctttgccctg aagcagaggg cagcctaagc 1080
 42 tcctgactcc agggaaatct ccctcccggg cttctctctc tcccggtcac cagtaacctc 1140
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 51 gattggcaga gtgaaatatt actgccgagg gaacgtagca gggcacacgt ctgcctctt 1680
 52 tgcgactcgg tgccccgttt ctccccatca cctacttact tcctggttgc aacctctctt 1740
 53 cctctgggac ttttgcaccg ggagctccag attcgctacc ccgcagcgct gcggagccgg 1800

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54 caggcagagg caccctgtac actgcagaga cccgaccctc cttgctacct tctagccaga 1860
55 actactgcag gctgattccc cctacacact ctctctgctc ttcccatgca aagcagaact 1920
56 ccgttgccctc aacgtccaac ccttctgcag ggctgcagtc cggccacccc aagaccttgc 1980
57 tgcaggggtgc ttcggatcc                                     1999
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61 <211> LENGTH: 20
62 <212> TYPE: DNA
63 <213> ORGANISM: artificial sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of the artificial sequence: Rev-DR2
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73 <211> LENGTH: 1845
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <220> FEATURE:
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79 <222> LOCATION: (1)..(1845)
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83 atg acg acc ctg gac tcc aac aac aac aca ggt ggc gtc atc acc tac 48
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85 1 5 10 15
87 att ggc tcc agt ggc tcc tcc cca agc cgc acc agc cct gaa tcc ctc 96
88 Ile Gly Ser Ser Gly Ser Ser Pro Ser Arg Thr Ser Pro Glu Ser Leu
89 20 25 30
91 tat agt gac aac tcc aat ggc agc ttc cag tcc ctg acc caa ggc tgt 144
92 Tyr Ser Asp Asn Ser Asn Gly Ser Phe Gln Ser Leu Thr Gln Gly Cys
93 35 40 45
95 ccc acc tac ttc cca cca tcc ccc act ggc tcc ctc acc caa gac ccg 192
96 Pro Thr Tyr Phe Pro Pro Ser Pro Thr Gly Ser Leu Thr Gln Asp Pro
97 50 55 60
99 gct cgc tcc ttt ggg agc att cca ccc agc ctg agt gat gac ggc tcc 240
100 Ala Arg Ser Phe Gly Ser Ile Pro Pro Ser Leu Ser Asp Asp Gly Ser
101 65 70 75 80
103 cct tct tcc tca tct tcc tcg tcg tca tcc tcc tcc tcc ttc tat aat 288
104 Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Phe Tyr Asn
105 85 90 95
107 ggg agc ccc cct ggg agt cta caa gtg gcc atg gag gac agc agc cga 336
108 Gly Ser Pro Pro Gly Ser Leu Gln Val Ala Met Glu Asp Ser Ser Arg
109 100 105 110
111 gtg tcc ccc agc aag agc acc agc aac atc acc aag ctg aat ggc atg 384
112 Val Ser Pro Ser Lys Ser Thr Ser Asn Ile Thr Lys Leu Asn Gly Met
113 115 120 125
115 gtg tta ctg tgt aaa gtg tgt ggg gac gtt gcc tcg ggc ttc cac tac 432
116 Val Leu Leu Cys Lys Val Cys Gly Asp Val Ala Ser Gly Phe His Tyr
117 130 135 140
119 ggt gtg cac gcc tgc gag ggc tgc aag ggc ttt ttc cgt cgg agc atc 480

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| 120 | Gly | Val | His | Ala | Cys | Glu | Gly | Cys | Lys | Gly | Phe | Phe | Arg | Arg | Ser | Ile | |
| 121 | 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| 123 | cag | cag | aac | atc | cag | tac | aaa | agg | tgt | ctg | aag | aat | gag | aat | tgc | tcc | 528 |
| 124 | Gln | Gln | Asn | Ile | Gln | Tyr | Lys | Arg | Cys | Leu | Lys | Asn | Glu | Asn | Cys | Ser | |
| 125 | | | | | 165 | | | | | 170 | | | | | | 175 | |
| 127 | atc | gtc | cgc | atc | aat | cgc | aac | cgc | tgc | cag | caa | tgt | cgc | ttc | aag | aag | 576 |
| 128 | Ile | Val | Arg | Ile | Asn | Arg | Asn | Arg | Cys | Gln | Gln | Cys | Arg | Phe | Lys | Lys | |
| 129 | | | | | 180 | | | | | 185 | | | | | | 190 | |
| 131 | tgt | ctc | tct | gtg | ggc | atg | tct | cga | gac | gct | gtg | cgt | ttt | ggg | cgc | atc | 624 |
| 132 | Cys | Leu | Ser | Val | Gly | Met | Ser | Arg | Asp | Ala | Val | Arg | Phe | Gly | Arg | Ile | |
| 133 | | | | | 195 | | | | 200 | | | | 205 | | | | |
| 135 | ccc | aaa | cga | gag | aag | cag | cgg | atg | ctt | gct | gag | atg | cag | agt | gcc | atg | 672 |
| 136 | Pro | Lys | Arg | Glu | Lys | Gln | Arg | Met | Leu | Ala | Glu | Met | Gln | Ser | Ala | Met | |
| 137 | | 210 | | | | | | 215 | | | | | 220 | | | | |
| 139 | aac | ctg | gcc | aac | aac | cag | ttg | agc | agc | cag | tgc | ccg | ctg | gag | act | tca | 720 |
| 140 | Asn | Leu | Ala | Asn | Asn | Gln | Leu | Ser | Ser | Gln | Cys | Pro | Leu | Glu | Thr | Ser | |
| 141 | 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| 143 | ccc | acc | cag | cac | ccc | acc | cca | ggc | ccc | atg | ggc | ccc | tcg | cca | ccc | cct | 768 |
| 144 | Pro | Thr | Gln | His | Pro | Thr | Pro | Gly | Pro | Met | Gly | Pro | Ser | Pro | Pro | Pro | |
| 145 | | | | | 245 | | | | | 250 | | | | | | 255 | |
| 147 | gct | ccg | gtc | ccc | tca | ccc | ctg | gtg | ggc | ttc | tcc | cag | ttt | cca | caa | cag | 816 |
| 148 | Ala | Pro | Val | Pro | Ser | Pro | Leu | Val | Gly | Phe | Ser | Gln | Phe | Pro | Gln | Gln | |
| 149 | | | | | 260 | | | | | 265 | | | | | | 270 | |
| 151 | ctg | acg | cct | ccc | aga | tcc | cca | agc | cct | gag | ccc | aca | gtg | gag | gat | gtg | 864 |
| 152 | Leu | Thr | Pro | Pro | Arg | Ser | Pro | Ser | Pro | Glu | Pro | Thr | Val | Glu | Asp | Val | |
| 153 | | | | | 275 | | | | 280 | | | | | | | 285 | |
| 155 | ata | tcc | cag | gtg | gcc | cgg | gcc | cat | cga | gag | atc | ttc | acc | tac | gcc | cat | 912 |
| 156 | Ile | Ser | Gln | Val | Ala | Arg | Ala | His | Arg | Glu | Ile | Phe | Thr | Tyr | Ala | His | |
| 157 | | 290 | | | | | | 295 | | | | 300 | | | | | |
| 159 | gac | aag | ctg | ggc | agc | tca | cct | ggc | aac | ttc | aat | gcc | aac | cat | gca | tca | 960 |
| 160 | Asp | Lys | Leu | Gly | Ser | Ser | Pro | Gly | Asn | Phe | Asn | Ala | Asn | His | Ala | Ser | |
| 161 | 305 | | | | | 310 | | | | 315 | | | | | | 320 | |
| 163 | ggt | agc | cct | cca | gcc | acc | acc | cca | cat | cgc | tgg | gaa | aat | cag | ggc | tgc | 1008 |
| 164 | Gly | Ser | Pro | Pro | Ala | Thr | Thr | Pro | His | Arg | Trp | Glu | Asn | Gln | Gly | Cys | |
| 165 | | | | | 325 | | | | | 330 | | | | | | 335 | |
| 167 | cca | cct | gcc | ccc | aat | gac | aac | aac | acc | ttg | gct | gcc | cag | cgt | cat | aac | 1056 |
| 168 | Pro | Pro | Ala | Pro | Asn | Asp | Asn | Asn | Thr | Leu | Ala | Ala | Gln | Arg | His | Asn | |
| 169 | | | | | 340 | | | | | 345 | | | | | | 350 | |
| 171 | gag | gcc | cta | aat | ggt | ctg | cgc | cag | gct | ccc | tcc | tcc | tac | cct | ccc | acc | 1104 |
| 172 | Glu | Ala | Leu | Asn | Gly | Leu | Arg | Gln | Ala | Pro | Ser | Ser | Tyr | Pro | Pro | Thr | |
| 173 | | | | | 355 | | | | 360 | | | | | | | 365 | |
| 175 | tgg | cct | cct | ggc | cct | gca | cac | agc | tgc | cac | cag | tcc | aac | agc | aac | | 1152 |
| 176 | Trp | Pro | Pro | Gly | Pro | Ala | His | Ser | Cys | His | Gln | Ser | Asn | Ser | Asn | | |
| 177 | | 370 | | | | | | 375 | | | | 380 | | | | | |
| 179 | ggg | cac | cgt | cta | tgc | ccc | acc | cac | gtg | tat | gca | gcc | cca | gaa | ggc | aag | 1200 |
| 180 | Gly | His | Arg | Leu | Cys | Pro | Thr | His | Val | Tyr | Ala | Ala | Pro | Glu | Gly | Lys | |
| 181 | 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| 183 | gca | cct | gcc | aac | agt | ccc | cgg | cag | ggc | aac | tca | aag | aat | gtt | ctg | ctg | 1248 |
| 184 | Ala | Pro | Ala | Asn | Ser | Pro | Arg | Gln | Gly | Asn | Ser | Lys | Asn | Val | Leu | Leu | |

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187 gca tgt cct atg aac atg tac ccg cat gga cgc agt ggg cga acg gtg 1296
188 Ala Cys Pro Met Asn Met Tyr Pro His Gly Arg Ser Gly Arg Thr Val
189          420          425          430
191 cag gag atc tgg gag gat ttc tcc atg agc ttc acg ccc gct gtg cgg 1344
192 Gln Glu Ile Trp Glu Asp Phe Ser Met Ser Phe Thr Pro Ala Val Arg
193          435          440          445
195 gag gtg gta gag ttt gcc aaa cac atc ccg ggc ttc cgt gac ctt tct 1392
196 Glu Val Val Glu Phe Ala Lys His Ile Pro Gly Phe Arg Asp Leu Ser
197          450          455          460
199 cag cat gac caa gtc acc ctg ctt aag gct ggc acc ttt gag gtg ctg 1440
200 Gln His Asp Gln Val Thr Leu Leu Lys Ala Gly Thr Phe Glu Val Leu
201 465          470          475          480
203 atg gtg cgc ttt gct tgc ttg ttc aac gtg aag gac cag aca gtg atg 1488
204 Met Val Arg Phe Ala Ser Leu Phe Asn Val Lys Asp Gln Thr Val Met
205          485          490          495
207 ttc cta agc cgc acc acc tac agc ctg cag gag ctt ggt gcc atg ggc 1536
208 Phe Leu Ser Arg Thr Thr Tyr Ser Leu Gln Glu Leu Gly Ala Met Gly
209          500          505          510
211 atg gga gac ctg ctc agt gcc atg ttc gac ttc agc gag aag ctc aac 1584
212 Met Gly Asp Leu Leu Ser Ala Met Phe Asp Phe Ser Glu Lys Leu Asn
213          515          520          525
215 tcc ctg gcg ctt acc gag gag gag ctg ggc ctc ttc acc gcg gtg gtg 1632
216 Ser Leu Ala Leu Thr Glu Glu Glu Leu Gly Leu Phe Thr Ala Val Val
217          530          535          540
219 ctt gtc tct gca gac cgc tgc ggc atg gag aat tcc gct tgc gtg gag 1680
220 Leu Val Ser Ala Asp Arg Ser Gly Met Glu Asn Ser Ala Ser Val Glu
221 545          550          555          560
223 cag ctc cag gag acg ctg ctg cgg gct ctt cgg gct ctg gtg ctg aag 1728
224 Gln Leu Gln Glu Thr Leu Leu Arg Ala Leu Arg Ala Leu Val Leu Lys
225          565          570          575
227 aac cgg ccc ttg gag act tcc cgc ttc acc aag ctg ctg ctc aag ctg 1776
228 Asn Arg Pro Leu Glu Thr Ser Arg Phe Thr Lys Leu Leu Leu Lys Leu
229          580          585          590
231 ccg gac ctg cgg acc ctg aac aac atg cat tcc gag aag ctg ctg tcc 1824
232 Pro Asp Leu Arg Thr Leu Asn Asn Met His Ser Glu Lys Leu Leu Ser
233          595          600          605
235 ttc cgg gtg gac gcc cag tga 1845
236 Phe Arg Val Asp Ala Gln
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242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 4
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247 1          5          10          15
248 Ile Gly Ser Ser Gly Ser Ser Pro Ser Arg Thr Ser Pro Glu Ser Leu
249          20          25          30

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252 Pro Thr Tyr Phe Pro Pro Ser Pro Thr Gly Ser Leu Thr Gln Asp Pro
253          50          55          60
254 Ala Arg Ser Phe Gly Ser Ile Pro Pro Ser Leu Ser Asp Asp Gly Ser
255 65          70          75          80
256 Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Phe Tyr Asn
257          85          90          95
258 Gly Ser Pro Pro Gly Ser Leu Gln Val Ala Met Glu Asp Ser Ser Arg
259          100          105          110
260 Val Ser Pro Ser Lys Ser Thr Ser Asn Ile Thr Lys Leu Asn Gly Met
261          115          120          125
262 Val Leu Leu Cys Lys Val Cys Gly Asp Val Ala Ser Gly Phe His Tyr
263          130          135          140
264 Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile
265 145          150          155          160
266 Gln Gln Asn Ile Gln Tyr Lys Arg Cys Leu Lys Asn Glu Asn Cys Ser
267          165          170          175
268 Ile Val Arg Ile Asn Arg Asn Arg Cys Gln Gln Cys Arg Phe Lys Lys
269          180          185          190
270 Cys Leu Ser Val Gly Met Ser Arg Asp Ala Val Arg Phe Gly Arg Ile
271          195          200          205
272 Pro Lys Arg Glu Lys Gln Arg Met Leu Ala Glu Met Gln Ser Ala Met
273          210          215          220
274 Asn Leu Ala Asn Asn Gln Leu Ser Ser Gln Cys Pro Leu Glu Thr Ser
275 225          230          235          240
276 Pro Thr Gln His Pro Thr Pro Gly Pro Met Gly Pro Ser Pro Pro Pro
277          245          250          255
278 Ala Pro Val Pro Ser Pro Leu Val Gly Phe Ser Gln Phe Pro Gln Gln
279          260          265          270
280 Leu Thr Pro Pro Arg Ser Pro Ser Pro Glu Pro Thr Val Glu Asp Val
281          275          280          285
282 Ile Ser Gln Val Ala Arg Ala His Arg Glu Ile Phe Thr Tyr Ala His
283          290          295          300
284 Asp Lys Leu Gly Ser Ser Pro Gly Asn Phe Asn Ala Asn His Ala Ser
285 305          310          315          320
286 Gly Ser Pro Pro Ala Thr Thr Pro His Arg Trp Glu Asn Gln Gly Cys
287          325          330          335
288 Pro Pro Ala Pro Asn Asp Asn Asn Thr Leu Ala Ala Gln Arg His Asn
289          340          345          350
290 Glu Ala Leu Asn Gly Leu Arg Gln Ala Pro Ser Ser Tyr Pro Pro Thr
291          355          360          365
292 Trp Pro Pro Gly Pro Ala His His Ser Cys His Gln Ser Asn Ser Asn
293          370          375          380
294 Gly His Arg Leu Cys Pro Thr His Val Tyr Ala Ala Pro Glu Gly Lys
295 385          390          395          400
297 Ala Pro Ala Asn Ser Pro Arg Gln Gly Asn Ser Lys Asn Val Leu Leu
298          405          410          415
299 Ala Cys Pro Met Asn Met Tyr Pro His Gly Arg Ser Gly Arg Thr Val

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date